#11

SEQUENCE LISTING

<110> Kindsvogel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827
<151> 2000-08-08

<150> US 60/250,876
<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 4.0

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<213> Homo sapien

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<221> CDS
<222> (34)...(1755)

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                                      Met Arg Thr Leu Leu Thr Ile
                                       1               5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat   102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
          10                  15                  20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg   150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
      25                  30                  35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc   198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
 40                  45                  50                  55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt   246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
                 60                  65                  70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac   294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
             75                  80                  85

ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc   342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
          90                  95                 100

cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act   390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr
     105                 110                 115

acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att   438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
120                 125                 130                 135
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cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc   486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly
                140                 145                 150

cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta   534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu
            155                 160                 165

gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag   582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln
        170                 175                 180

aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc   630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly
    185                 190                 195

acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac   678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr
200                 205                 210                 215

atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc   726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe
                220                 225                 230

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc   774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys
            235                 240                 245

tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc   822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser
        250                 255                 260

ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag   870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln
    265                 270                 275

gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg   918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu
280                 285                 290                 295

gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag   966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu
                300                 305                 310

ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta  1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu
            315                 320                 325

ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc  1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro
        330                 335                 340

cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc  1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val
    345                 350                 355

ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca  1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro
360                 365                 370                 375

ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc  1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
                380                 385                 390

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg  1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
            395                 400                 405

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa  1302
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Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
        410                 415                 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc   1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
    425                 430                 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg   1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
440                 445                 450                 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc   1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
                460                 465                 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg   1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
            475                 480                 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag   1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
        490                 495                 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca   1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
    505                 510                 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc   1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
520                 525                 530                 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca   1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
                540                 545                 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc   1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
            555                 560                 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc      1785
Leu Thr Val Gln Trp Glu Ser
        570

tccctgtccc tacccagtgt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag 1905
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<212> PRT
<213> Homo sapien

<400> 2
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
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            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
225                 230                 235                 240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
                245                 250                 255
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
            260                 265                 270
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
        275                 280                 285
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
    290                 295                 300
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
305                 310                 315                 320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
                325                 330                 335
Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
            340                 345                 350
Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
        355                 360                 365
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
    370                 375                 380
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
385                 390                 395                 400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
                405                 410                 415
Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
            420                 425                 430
Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
        435                 440                 445
Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
    450                 455                 460
His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
465                 470                 475                 480
Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
                485                 490                 495
Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
            500                 505                 510
Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
        515                 520                 525
Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
    530                 535                 540
Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
545                 550                 555                 560
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Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
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<210> 3
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<212> PRT
<213> Homo sapiens

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            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
        35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
                85                  90                  95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
            100                 105                 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
        115                 120                 125
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
    130                 135                 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145                 150                 155                 160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
                165                 170                 175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
            180                 185                 190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
        195                 200                 205
Thr Trp Thr
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<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu peptide tag

<400> 4
Glu Tyr Met Pro Met Glu
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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag-tag peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5


<210> 6
<211> 699
<212> DNA
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<213> Homo sapiens

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ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
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<220>
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<222> (21)...(557)

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Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
15 20 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
30 35 40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
80 85 90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
110 115 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
160 165 170

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atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac  587
Met Ser Leu Arg Asn Ala Cys Ile
            175

taacccccct tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt 827
atttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
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acatcattcg atattgctac ttgagtgtaa ggctaatatt gatatttatg acaataatta 1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta              1116

<210> 8
<211> 179
<212> PRT
<213> homo sapiens

<400> 8
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Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
            20                  25                  30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
        35                  40                  45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
    50                  55                  60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65                  70                  75                  80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
                85                  90                  95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
            100                 105                 110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
        115                 120                 125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
    130                 135                 140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145                 150                 155                 160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165                 170                 175
Ala Cys Ile



<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC28590

<400> 9
ttgggtacct ctgcaatggc cgccctgcag aaatct                           36

<210> 10
<211> 33
<212> DNA
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<220>
<223> Oligonucleotide prime ZC28580

<400> 10
ttgggatcca atgcaggcat ttctcagaga cat                              33
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<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC14666

<400> 11
agccaccaag atgactga 18

<210> 12
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<212> DNA
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<220>
<223> Oligonucleotide prime ZC14742

<400> 12
tgcatttggt aggtgcggtt ga 22

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 13
His His His His His His
1 5

<210> 14
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29239

<400> 14
gaggccggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29232

<400> 15
cgactgactc gagtcagtga tggtgatggt gatggccacc tgatccttta cccggagaca 60
gggag 65

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39319

<400> 16
atcggaattc gcagaagcca tggcgtggag ccttggg 37

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39325

<400> 17
cagtggatcc ggaggggacc gtttcgtc 28

<210> 18
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(660)

<400> 18
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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt   96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg   144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat   192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc   240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag   288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att   336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat   384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act   432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa   480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag   528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga   576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
```

```
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc   624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc                   660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220
```

<210> 19
<211> 220
<212> PRT
<213> Homo sapiens

<400> 19

```
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220
```

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC38931

<400> 20

```
acaaagccgc gggaggag                                               18
```

<210> 21
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39042

<400> 21

```
ctgactcgag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca 60
gtttacccgg agacagggag ag                                           82
```

<210> 22
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
to IgGg1 with a 6-HIS tag

<400> 22

```
atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca   48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt   96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg   144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat   192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc   240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag   288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att   336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat   384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act   432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa   480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag   528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga   576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc   624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg   672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
    210                 215                 220
```

```
ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca   720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240

ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc   768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc   816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc   864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        275                 280                 285

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg   912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    290                 295                 300

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc   960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305                 310                 315                 320

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc  1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                325                 330                 335

tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc  1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg  1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
        355                 360                 365

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc  1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    370                 375                 380

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg  1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385                 390                 395                 400

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc  1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405                 410                 415

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag  1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420                 425                 430

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac  1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt  1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
    450                 455                 460

ggt tcc gga tca ggt ggc cat cac cat cac cat cac                  1428
Gly Ser Gly Ser Gly Gly His His His His His His
465                 470                 475
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<210> 23
<211> 476
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
115 120 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
195 200 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
210 215 220
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225 230 235 240
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
245 250 255
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
260 265 270
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
275 280 285
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
290 295 300
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305 310 315 320
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
325 330 335
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
340 345 350
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
355 360 365
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
370 375 380
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385 390 395 400
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
405 410 415
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
420 425 430
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
435 440 445
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
450 455 460
Gly Ser Gly Ser Gly Gly His His His His His His
465 470 475

<210> 24
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29328

<400> 24
tcagagggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 25
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29231

<400> 25
cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60
gggag 65

<210> 26
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39335

<400> 26
atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC28981

<400> 27
tttgggctcc ctgagctctg gtggaa 26

<210> 28
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39043

<400> 28
ctgactcgag ctactccata ggcatatact cgccacctga tccggaacca cgcggaacca 60
gtttacccgg agacagggag 80

<210> 29
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> hzcytor11 extracellular cytokine binding domain
fused to IgGg1 with a Glu-Glu tag

<221> CDS
<222> (1)...(1452)

<400> 29
atg agg acg ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac 48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His

```
                                                    15
 1               5                  10                  15

gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg aaa ttc cag tcc   96
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30

agc aac ttt gaa aac atc ctg acg tgg gac agc ggg cca gag ggc acc  144
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45

cca gac acg gtc tac agc atc gag tat aag acg tac gga gag agg gac  192
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60

tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg aag tcc tgc aac  240
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80

ctg acg gtg gag acg ggc aac ctc acg gag ctc tac tat gcc agg gtc  288
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95

acc gct gtc agt gcg gga ggc cgg tca gcc acc aag atg act gac agg  336
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110

ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt  384
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125

atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg  432
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140

cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc  480
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160

cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa  528
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175

atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc  576
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190

cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg  624
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205

gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac  672
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220

cgg aca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca  720
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240

tca gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag  768
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255

ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc  816
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc  864
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
```

```
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag   912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg   960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat   1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc   1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag   1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365

gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc   1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg   1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct   1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc   1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg   1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg   1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat   1440
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480

atg cct atg gag                                                  1452
Met Pro Met Glu
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<210> 30
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide encoded by the hzcytor11 extracellular cytokine binding domain fused to IgGg1 with a Glu-Glu tag of SEQ ID NO: 29

<400> 30

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Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1               5                  10                  15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
```

```
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480
Met Pro Met Glu
```

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37693

<400> 31

ccccagacac ggtctacagc at 22

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37449

<400> 32
gggtcaggcc gaagaactca tat 23

<210> 33
<211> 199
<212> PRT
<213> Homo sapiens

<400> 33

Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys
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Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
			20					25					30		
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
		35					40					45			
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
	50					55					60				
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65					70					75					80
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
				85					90					95	
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
			100					105					110		
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
		115					120					125			
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
	130					135					140				
Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	Val	Leu	Arg
145					150					155					160
Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	Gly	Phe	Leu
				165					170					175	
Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	Cys	Glu	Gln
			180					185					190		
Thr	Thr	His	Asp	Glu	Thr	Val									
		195													

<210> 34
<211> 211
<212> PRT
<213> Homo sapiens

<400> 34

Ser	Asp	Ala	His	Gly	Thr	Glu	Leu	Pro	Ser	Pro	Pro	Ser	Val	Trp	Phe
1				5					10					15	
Glu	Ala	Glu	Phe	Phe	His	His	Ile	Leu	His	Trp	Thr	Pro	Ile	Pro	Asn
			20					25					30		
Gln	Ser	Glu	Ser	Thr	Cys	Tyr	Glu	Val	Ala	Leu	Leu	Arg	Tyr	Gly	Ile
		35					40					45			
Glu	Ser	Trp	Asn	Ser	Ile	Ser	Asn	Cys	Ser	Gln	Thr	Leu	Ser	Tyr	Asp
	50					55					60				
Leu	Thr	Ala	Val	Thr	Leu	Asp	Leu	Tyr	His	Ser	Asn	Gly	Tyr	Arg	Ala
65					70					75					80
Arg	Val	Arg	Ala	Val	Asp	Gly	Ser	Arg	His	Ser	Asn	Trp	Thr	Val	Thr
				85					90					95	
Asn	Thr	Arg	Phe	Ser	Val	Asp	Glu	Val	Thr	Leu	Thr	Val	Gly	Ser	Val
			100					105					110		
Asn	Leu	Glu	Ile	His	Asn	Gly	Phe	Ile	Leu	Gly	Lys	Ile	Gln	Leu	Pro
		115					120					125			

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Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
    130                 135                 140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145                 150                 155                 160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
                165                 170                 175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
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Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
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Thr Arg Gln
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Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
            20                  25                  30
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
        35                  40                  45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
    50                  55                  60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65                  70                  75                  80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
                85                  90                  95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
            100                 105                 110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
        115                 120                 125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
    130                 135                 140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145                 150                 155                 160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
                165                 170                 175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
            180                 185                 190
Glu Cys Val Glu Val Gln Gly Glu Ala
        195                 200
```